

RAW SEQUENCE LISTING

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Application Serial Number: 10/550,768
Source: PCT
Date Processed by STIC: 10/07/2005

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PCT

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DATE: 10/07/2005

PATENT APPLICATION: US/10/550,768

TIME: 09:30:19

Input Set : A:\298641 sequence listing.txt

Output Set: N:\CRF4\10072005\J550768.raw

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4 <110> APPLICANT: Meritet, Jean-Francois
5      Dron, Michel
6      Tovey, Michael Gerard
9 <120> TITLE OF INVENTION: INTERFERON-ALPHA INDUCED GENE
11 <130> FILE REFERENCE: 046658/298641
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/550,768
C--> 13 <141> CURRENT FILING DATE: 2005-09-27
13 <160> NUMBER OF SEQ ID NOS: 2
15 <170> SOFTWARE: PatentIn version 3.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 6045
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (243)..(5381)
27 <223> OTHER INFORMATION:
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31 agcgggctgg gtcctaggcc aggtctgggg taacctggaa cttccacctg ggctctgcgc      60
32 taggtctctg tttcactccc tccccgcggg gcgcgcagct cgcgggtctt tggacaccac      120
33 cggtcctgag tccgcggact gccattttca ttaagaactg ccacttagag gtaccaaatt      180
34 aaaggggtatt tgctaccttt aatacttgcc agttcagggt ggaggcacag gcagcagcaa      240
36 ga atg gaa aga aat gtt ctt aca aca ttt tca cag gaa atg tcc cag      287
37   Met Glu Arg Asn Val Leu Thr Thr Phe Ser Gln Glu Met Ser Gln
38   1           5           10          15
40 tta att ttg aat gaa atg cca aaa gct gaa tat tcc agt tta ttc aat      335
41 Leu Ile Leu Asn Glu Met Pro Lys Ala Glu Tyr Ser Ser Leu Phe Asn
42           20           25           30
44 gat ttt gtt gaa tct gaa ttt ttt ttg att gat ggg gat tca tta ctt      383
45 Asp Phe Val Glu Ser Glu Phe Phe Leu Ile Asp Gly Asp Ser Leu Leu
46           35           40           45
48 atc aca tgt atc tgt gag ata tca ttt aag cct ggg cag aac ctc cat      431
49 Ile Thr Cys Ile Cys Glu Ile Ser Phe Lys Pro Gly Gln Asn Leu His
50           50           55           60
52 ttc ttc tat ctg gtt gaa cgc tat ctt gtg gat ctt att agc aaa gga      479
53 Phe Phe Tyr Leu Val Glu Arg Tyr Leu Val Asp Leu Ile Ser Lys Gly
54           65           70           75
56 gga caa ttc acc ata gtt ttc ttc aag gat gcc gag tat gcg tat ttc      527
57 Gly Gln Phe Thr Ile Val Phe Phe Lys Asp Ala Glu Tyr Ala Tyr Phe
58 80           85           90           95
59 aac ttc cct gaa ctt ctt tct ttg aga act gct tta att ctt cat ctt      575
60 Asn Phe Pro Glu Leu Leu Ser Leu Arg Thr Ala Leu Ile Leu His Leu
61           100          105          110

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63	cag aag aat acc acc att gat gtt cga aca aca ttt tcg aga tgc tta	623
64	Gln Lys Asn Thr Thr Ile Asp Val Arg Thr Thr Phe Ser Arg Cys Leu	
65	115 120 125	
67	tca aaa gag tgg gga agt ttc ttg gaa gag agt tac cca tat ttc ctg	671
68	Ser Lys Glu Trp Gly Ser Phe Leu Glu Glu Ser Tyr Pro Tyr Phe Leu	
69	130 135 140	
71	ata gtt gca gac gaa ggc ctg aac gat cta caa aca cag ctt ttc aac	719
72	Ile Val Ala Asp Glu Gly Leu Asn Asp Leu Gln Thr Gln Leu Phe Asn	
73	145 150 155	
75	ttt tta atc att cat tct tgg gca agg aag gtc aac gtt gta ctt tcc	767
76	Phe Leu Ile Ile His Ser Trp Ala Arg Lys Val Asn Val Val Leu Ser	
77	160 165 170 175	
79	tca ggg caa gaa tct gat gtt ctt tgc ctt tat gca tac ctt ctt cca	815
80	Ser Gly Gln Glu Ser Asp Val Leu Cys Leu Tyr Ala Tyr Leu Leu Pro	
81	180 185 190	
83	agc atg tac aga cac cag att ttt tcc tgg aag aat aag cag aac att	863
84	Ser Met Tyr Arg His Gln Ile Phe Ser Trp Lys Asn Lys Gln Asn Ile	
85	195 200 205	
87	aaa gat gct tat aca acc ctg ctt aac cag ttg gaa aga ttt aag ctt	911
88	Lys Asp Ala Tyr Thr Thr Leu Leu Asn Gln Leu Glu Arg Phe Lys Leu	
89	210 215 220	
91	tca gca tta gca cct ctt ttt gga agt tta aaa tgg aat aat att acg	959
92	Ser Ala Leu Ala Pro Leu Phe Gly Ser Leu Lys Trp Asn Asn Ile Thr	
93	225 230 235	
95	gaa gag gca cac aag act gta tct ctg ctt aca caa gtc tgg cca gaa	1007
96	Glu Glu Ala His Lys Thr Val Ser Leu Leu Thr Gln Val Trp Pro Glu	
97	240 245 250 255	
99	gga tct gac att cgg cgt gtc ttt tgt gtt act tca tgc tca tta tct	1055
100	Gly Ser Asp Ile Arg Arg Val Phe Cys Val Thr Ser Cys Ser Leu Ser	
101	260 265 270	
103	ttg aga atg tac cat cgc ttt tta gga aac aga gag ccc tcc tct ggt	1103
104	Leu Arg Met Tyr His Arg Phe Leu Gly Asn Arg Glu Pro Ser Ser Gly	
105	275 280 285	
107	cag gaa act gag atc caa cag gtg aac agt aat tgc tta acc ctg cag	1151
108	Gln Glu Thr Glu Ile Gln Gln Val Asn Ser Asn Cys Leu Thr Leu Gln	
109	290 295 300	
110	gag atg gaa gat ttg tgt aaa ctg cat tgt ctc act gtg gtt ttt cta	1199
111	Glu Met Glu Asp Leu Cys Lys Leu His Cys Leu Thr Val Val Phe Leu	
112	305 310 315	
114	ctc cat ctg cct ctt tct caa aga gct tgt gct aga gtc atc act tcc	1247
115	Leu His Leu Pro Leu Ser Gln Arg Ala Cys Ala Arg Val Ile Thr Ser	
116	320 325 330 335	
118	cat tgg gct gag gac atg aag cct tta tta caa atg aaa aag tgg tgt	1295
119	His Trp Ala Glu Asp Met Lys Pro Leu Leu Gln Met Lys Lys Trp Cys	
120	340 345 350	
122	gaa tat ttc atc tta aga aat ata cat act ttt gaa ttt tgg aat ctg	1343
123	Glu Tyr Phe Ile Leu Arg Asn Ile His Thr Phe Glu Phe Trp Asn Leu	
124	355 360 365	
126	aat tta att cac ctt tct gac tta aat gat gag ctt ttg ttg aag aat	1391

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127 Asn Leu Ile His Leu Ser Asp Leu Asn Asp Glu Leu Leu Leu Lys Asn
128      370      375      380
130 att gct ttt tac tat gaa aat gaa aat gta aaa ggc cta cat ttg aat      1439
131 Ile Ala Phe Tyr Tyr Glu Asn Glu Asn Val Lys Gly Leu His Leu Asn
132      385      390      395
134 ttg gga gat acc att atg aaa gat tat gaa tat ctc tgg aat acc gta      1487
135 Leu Gly Asp Thr Ile Met Lys Asp Tyr Glu Tyr Leu Trp Asn Thr Val
136 400      405      410      415
138 tca aag ttg gtc aga gac ttt gag gtt gga cag cca ttt cct ctg aga      1535
139 Ser Lys Leu Val Arg Asp Phe Glu Val Gly Gln Pro Phe Pro Leu Arg
140      420      425      430
142 aca aca aaa gtt tgt ttt ctt gga aag aaa cca tca cca atc aaa gac      1583
143 Thr Thr Lys Val Cys Phe Leu Gly Lys Lys Pro Ser Pro Ile Lys Asp
144      435      440      445
146 agc tcc aat gaa atg gtg ccc aat ttg ggt ttt att cca acg tca tct      1631
147 Ser Ser Asn Glu Met Val Pro Asn Leu Gly Phe Ile Pro Thr Ser Ser
148      450      455      460
150 ttt gtg gtt gat aaa ttt gct gga gat att ttg aaa gat ttg cct ttt      1679
151 Phe Val Val Asp Lys Phe Ala Gly Asp Ile Leu Lys Asp Leu Pro Phe
152      465      470      475
154 cta aag agt gat gat cct att gtt act tca ctg gtt aaa caa aag gaa      1727
155 Leu Lys Ser Asp Asp Pro Ile Val Thr Ser Leu Val Lys Gln Lys Glu
156 480      485      490      495
158 ttt gat gaa ctt gtg cac tgg cat tct cat aaa ccc ctg agt gat gat      1775
159 Phe Asp Glu Leu Val His Trp His Ser His Lys Pro Leu Ser Asp Asp
160      500      505      510
161 tat gac agg tcc agg tgt cag ttt gat gaa aaa tct aga gac cct cgt      1823
162 Tyr Asp Arg Ser Arg Cys Gln Phe Asp Glu Lys Ser Arg Asp Pro Arg
163      515      520      525
165 gtt ctt aga tct gtg caa aag tat cat gtt ttc caa cgg ttt tat ggg      1871
166 Val Leu Arg Ser Val Gln Lys Tyr His Val Phe Gln Arg Phe Tyr Gly
167      530      535      540
169 aat tca tta gaa aca gtc tct tcg aaa atc atc gtg act caa act att      1919
170 Asn Ser Leu Glu Thr Val Ser Ser Lys Ile Ile Val Thr Gln Thr Ile
171      545      550      555
173 aag tca aag aag gat ttt agt ggg ccc aag agc aaa aag gca cac gag      1967
174 Lys Ser Lys Lys Asp Phe Ser Gly Pro Lys Ser Lys Lys Ala His Glu
175 560      565      570      575
177 acc aag gct gaa ata att gct aga gag aat aag aaa agg tta ttt gcc      2015
178 Thr Lys Ala Glu Ile Ile Ala Arg Glu Asn Lys Lys Arg Leu Phe Ala
179      580      585      590
181 agg gaa gaa caa aag gaa gag caa aag tgg aat gct ttg tca ttt tct      2063
182 Arg Glu Glu Gln Lys Glu Glu Gln Lys Trp Asn Ala Leu Ser Phe Ser
183      595      600      605
185 att gaa gag caa ttg aaa gaa aat tta cac tct gga ata aag agc ctg      2111
186 Ile Glu Glu Gln Leu Lys Glu Asn Leu His Ser Gly Ile Lys Ser Leu
187      610      615      620
189 gaa gat ttt ttg aaa tcc tgt aaa agt agc tgt gtg aaa ctt cag gtt      2159
190 Glu Asp Phe Leu Lys Ser Cys Lys Ser Ser Cys Val Lys Leu Gln Val

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191      625      630      635
193 gaa atg gtg ggg tta act gct tgc ttg aaa gcc tgg aaa gaa cat tgc      2207
194 Glu Met Val Gly Leu Thr Ala Cys Leu Lys Ala Trp Lys Glu His Cys
195 640      645      650      655
197 cga agt gaa gaa ggt aaa acc acg aaa gat tta agt ata gct gtt cag      2255
198 Arg Ser Glu Glu Gly Lys Thr Thr Lys Asp Leu Ser Ile Ala Val Gln
199      660      665      670
201 gtg atg aaa agg atc cac tcc ttg atg gaa aaa tac tca gaa ctt tta      2303
202 Val Met Lys Arg Ile His Ser Leu Met Glu Lys Tyr Ser Glu Leu Leu
203      675      680      685
205 caa gaa gat gat cgg caa ctc ata gcc aga tgc ctt aag tat tta gga      2351
206 Gln Glu Asp Asp Arg Gln Leu Ile Ala Arg Cys Leu Lys Tyr Leu Gly
207      690      695      700
209 ttt gat gag ttg gca agt tct tta cat cca gcc cag gat gca gaa aat      2399
210 Phe Asp Glu Leu Ala Ser Ser Leu His Pro Ala Gln Asp Ala Glu Asn
211      705      710      715
212 gat gta aaa gtg aag aaa agg aat aaa tat tca att ggc att ggg cca      2447
213 Asp Val Lys Val Lys Lys Arg Asn Lys Tyr Ser Ile Gly Ile Gly Pro
214 720      725      730      735
216 gct cgg ttc caa ctg caa tac atg ggc cat tat ttg ata cga gat gag      2495
217 Ala Arg Phe Gln Leu Gln Tyr Met Gly His Tyr Leu Ile Arg Asp Glu
218      740      745      750
220 aga aaa gac cca gat ccc agg gtc cag gat ttt att ccc gac aca tgg      2543
221 Arg Lys Asp Pro Asp Pro Arg Val Gln Asp Phe Ile Pro Asp Thr Trp
222      755      760      765
224 cag cga gag ctc ctt gat gtt gtg gat aag aat gag tca gca gtg att      2591
225 Gln Arg Glu Leu Leu Asp Val Val Asp Lys Asn Glu Ser Ala Val Ile
226      770      775      780
228 gtt gcc cca acg tcc tca ggc aaa aca tat gcc tcc tac tac tgt atg      2639
229 Val Ala Pro Thr Ser Ser Gly Lys Thr Tyr Ala Ser Tyr Tyr Cys Met
230      785      790      795
232 gag aaa gtg ctg aag gag agc gac gac ggg gtg gtc gtg tac gtt gca      2687
233 Glu Lys Val Leu Lys Glu Ser Asp Asp Gly Val Val Val Tyr Val Ala
234 800      805      810      815
236 ccc aca aag gcc ctt gtt aat caa gtg gca gca act gtt cag aat cgt      2735
237 Pro Thr Lys Ala Leu Val Asn Gln Val Ala Ala Thr Val Gln Asn Arg
238      820      825      830
240 ttt acg aaa aat ctg cca agt ggt gaa gtt ctc tgt ggt gtt ttc acc      2783
241 Phe Thr Lys Asn Leu Pro Ser Gly Glu Val Leu Cys Gly Val Phe Thr
242      835      840      845
244 agg gag tat cgt cat gat gcc tta aac tgt cag gta ctt att aca gtg      2831
245 Arg Glu Tyr Arg His Asp Ala Leu Asn Cys Gln Val Leu Ile Thr Val
246      850      855      860
248 cct gcc tgc ttt gaa att ctg ctg ctt gct cct cat cgc caa aac tgg      2879
249 Pro Ala Cys Phe Glu Ile Leu Leu Leu Ala Pro His Arg Gln Asn Trp
250      865      870      875
252 gtg aaa aag atc aga tat gtt ata ttt gat gag gtt cat tgt ctt ggt      2927
253 Val Lys Lys Ile Arg Tyr Val Ile Phe Asp Glu Val His Cys Leu Gly
254 880      885      890      895

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256	gga gaa att gga gca gaa atc tgg gaa cat ctc ctt gtc atg atc cga	2975
257	Gly Glu Ile Gly Ala Glu Ile Trp Glu His Leu Leu Val Met Ile Arg	
258	900 905 910	
260	tgt ccc ttt ttg gct ctt tca gct acc ata agt aat cct gaa cat ctc	3023
261	Cys Pro Phe Leu Ala Leu Ser Ala Thr Ile Ser Asn Pro Glu His Leu	
262	915 920 925	
263	acc gag tgg cta caa tcg gta aaa tgg tac tgg aaa caa gaa gac aaa	3071
264	Thr Glu Trp Leu Gln Ser Val Lys Trp Tyr Trp Lys Gln Glu Asp Lys	
265	930 935 940	
267	ata att gaa aat aat acc gct tct aaa aga cat gtg ggt cgt cag gcc	3119
268	Ile Ile Glu Asn Asn Thr Ala Ser Lys Arg His Val Gly Arg Gln Ala	
269	945 950 955	
271	ggc ttt ccc aaa gac tac ttg caa gta aaa caa tcg tat aaa gtt aga	3167
272	Gly Phe Pro Lys Asp Tyr Leu Gln Val Lys Gln Ser Tyr Lys Val Arg	
273	960 965 970 975	
275	ctt gtg ctc tat gga gag agg tat aat gat cta gag aag cat gta tgt	3215
276	Leu Val Leu Tyr Gly Glu Arg Tyr Asn Asp Leu Glu Lys His Val Cys	
277	980 985 990	
279	tca ata aaa cat ggt gac att cat ttt gat cat ttt cac cca tgt gct	3263
280	Ser Ile Lys His Gly Asp Ile His Phe Asp His Phe His Pro Cys Ala	
281	995 1000 1005	
283	gca cta aca aca gat cat att gaa agg tat gga ttc cct cct gat	3308
284	Ala Leu Thr Thr Asp His Ile Glu Arg Tyr Gly Phe Pro Pro Asp	
285	1010 1015 1020	
287	ctt acc ctt tca cct cga gaa agc atc cag ctg tat gat gcc atg	3353
288	Leu Thr Leu Ser Pro Arg Glu Ser Ile Gln Leu Tyr Asp Ala Met	
289	1025 1030 1035	
291	ttt caa att tgg aaa agt tgg cct cgg gcc cag gaa ctg tgc cca	3398
292	Phe Gln Ile Trp Lys Ser Trp Pro Arg Ala Gln Glu Leu Cys Pro	
293	1040 1045 1050	
295	gaa aac ttc att cat ttt aac aat aaa tta gtc att aaa aag atg	3443
296	Glu Asn Phe Ile His Phe Asn Asn Lys Leu Val Ile Lys Lys Met	
297	1055 1060 1065	
299	gat gct agg aaa tat gaa gag agt cta aag gca gaa tta aca agt	3488
300	Asp Ala Arg Lys Tyr Glu Glu Ser Leu Lys Ala Glu Leu Thr Ser	
301	1070 1075 1080	
303	tgg att aaa aat ggc aac gta gag cag gcc aga atg gta ctt cag	3533
304	Trp Ile Lys Asn Gly Asn Val Glu Gln Ala Arg Met Val Leu Gln	
305	1085 1090 1095	
307	aat ctt agt cct gaa gca gat ttg agt cca gaa aac atg atc acc	3578
308	Asn Leu Ser Pro Glu Ala Asp Leu Ser Pro Glu Asn Met Ile Thr	
309	1100 1105 1110	
311	atg ttt cca ctt cta gtt gaa aaa cta agg aaa atg gag aag tta	3623
312	Met Phe Pro Leu Leu Val Glu Lys Leu Arg Lys Met Glu Lys Leu	
313	1115 1120 1125	
314	cct gca cta ttt ttt tta ttc aag tta gga gct gta gaa aac gca	3668
315	Pro Ala Leu Phe Phe Leu Phe Lys Leu Gly Ala Val Glu Asn Ala	
316	1130 1135 1140	
318	gct gaa agt gtg agc act ttc cta aag aaa aag cag gag aca aaa	3713

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:29 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27